



## SEQUENCE LISTING

<110> REGEN Biotech. Inc.

<120> The method for measuring the amount of Betaig - h 3 protein and diagnostic kit using the same

<130> 2fpo-10-14

<160> 12

<170> KopatentIn 1.71

<210> 1

<211> 683

<212> PRT

<213> Homo sapiens

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Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val  
35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn  
50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile  
65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly  
85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val  
100 105 110

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu  
115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser  
130 135 140

Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val  
145 150 155 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val  
 165 170 175

Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr  
 180 185 190

Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly  
 195 200 205

Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala  
 210 215 220

Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr  
 225 230 235 240

Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu  
 245 250 255

Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn  
 260 265 270

Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile  
 275 280 285

Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg  
 290 295 300

Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala  
 305 310 315 320

Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu  
 325 330 335

Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile  
 340 345 350

Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp  
 355 360 365

Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala  
 370 375 380

Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu  
 385 390 395 400

Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu  
 405 410 415

Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg

420	425	430
Asn Leu Leu Arg Asn His Ile Ile	Lys Asp Gln Leu Ala Ser Lys Tyr	
435	440	445
Leu Tyr His Gly Gln Thr Leu Glu Thr	Leu Gly Gly Lys Lys Leu Arg	
450	455	460
Val Phe Val Tyr Arg Asn Ser Leu Cys Ile	Glu Asn Ser Cys Ile Ala	
465	470	475
480		
Ala His Asp Lys Arg Gly Arg Tyr Gly Thr	Leu Phe Thr Met Asp Arg	
485	490	495
Val Leu Thr Pro Pro Met Gly Thr Val Met	Asp Val Leu Lys Gly Asp	
500	505	510
Asn Arg Phe Ser Met Leu Val Ala Ala Ile	Gln Ser Ala Gly Leu Thr	
515	520	525
Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr	Val Phe Ala Pro Thr Asn	
530	535	540
Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu	Arg Ser Arg Leu Leu Gly	
545	550	555
560		
Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys	Tyr His Ile Gly Asp Glu	
565	570	575
Ile Leu Val Ser Gly Gly Ile Gly Ala Leu	Val Arg Leu Lys Ser Leu	
580	585	590
Gln Gly Asp Lys Leu Glu Val Ser Leu Lys	Asn Asn Val Val Ser Val	
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Asn Lys Glu Pro Val Ala Glu Pro Asp Ile	Met Ala Thr Asn Gly Val	
610	615	620
Val His Val Ile Thr Asn Val Leu Gln Pro	Pro Ala Asn Arg Pro Gln	
625	630	635
640		
Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala	Leu Glu Ile Phe Lys Gln	
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Val Tyr Gln Lys Leu Leu Glu Arg Met Lys	His	
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<210> 2  
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 <212> DNA  
 <213> Homo sapiens

<400> 2

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<210> 3  
 <211> 585  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(585)  
 <223> 69 to 653 amino acid sequence of human ID No.1

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 20 25 30  
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 35 40 45  
 Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met  
 50 55 60  
 Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp  
 65 70 75 80  
 Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn  
 85 90 95  
 Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val  
 100 105 110  
 Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln  
 115 120 125  
 Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val  
 130 135 140  
 Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val  
 145 150 155 160  
 Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln  
 165 170 175  
 Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val  
 180 185 190

Ala	Ala	Ser	Gly	Leu	Asn	Thr	Met	Leu	Glu	Gly	Asn	Gly	Gln	Tyr	Thr	195	200	205	
Leu	Leu	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Ile	Pro	Ser	Glu	Thr	210	215	220	
Leu	Asn	Arg	Ile	Leu	Gly	Asp	Pro	Glu	Ala	Leu	Arg	Asp	Leu	Leu	Asn	225	230	235	240
Asn	His	Ile	Leu	Lys	Ser	Ala	Met	Cys	Ala	Glu	Ala	Ile	Val	Ala	Gly	245	250	255	
Leu	Ser	Val	Glu	Thr	Leu	Glu	Gly	Thr	Thr	Leu	Glu	Val	Gly	Cys	Ser	260	265	270	
Gly	Asp	Met	Leu	Thr	Ile	Asn	Gly	Lys	Ala	Ile	Ile	Ser	Asn	Lys	Asp	275	280	285	
Ile	Leu	Ala	Thr	Asn	Gly	Val	Ile	His	Tyr	Ile	Asp	Glu	Leu	Leu	Ile	290	295	300	
Pro	Asp	Ser	Ala	Lys	Thr	Leu	Phe	Glu	Leu	Ala	Ala	Glu	Ser	Asp	Val	305	310	315	320
Ser	Thr	Ala	Ile	Asp	Leu	Phe	Arg	Gln	Ala	Gly	Leu	Gly	Asn	His	Leu	325	330	335	
Ser	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Leu	Ala	Pro	Leu	Asn	Ser	Val	Phe	340	345	350	
Lys	Asp	Gly	Thr	Pro	Pro	Ile	Asp	Ala	His	Thr	Arg	Asn	Leu	Leu	Arg	355	360	365	
Asn	His	Ile	Ile	Lys	Asp	Gln	Leu	Ala	Ser	Lys	Tyr	Leu	Tyr	His	Gly	370	375	380	
Gln	Thr	Leu	Glu	Thr	Leu	Gly	Gly	Lys	Lys	Leu	Arg	Val	Phe	Val	Tyr	385	390	395	400
Arg	Asn	Ser	Leu	Cys	Ile	Glu	Asn	Ser	Cys	Ile	Ala	Ala	His	Asp	Lys	405	410	415	
Arg	Gly	Arg	Tyr	Gly	Thr	Leu	Phe	Thr	Met	Asp	Arg	Val	Leu	Thr	Pro	420	425	430	
Pro	Met	Gly	Thr	Val	Met	Asp	Val	Leu	Lys	Gly	Asp	Asn	Arg	Phe	Ser	435	440	445	
Met	Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu	Thr	Leu	Asn				

450		455		460
Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg				
465		470		475
				480
Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu				
	485		490	495
Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser				
	500		505	510
Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys				
	515		520	525
Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro				
	530		535	540
Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile				
	545		550	555
				560
Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln Glu Arg Gly Asp				
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Glu Leu Ala Asp Ser Ala Leu Glu Ile				
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<210> 4  
 <211> 1857  
 <212> DNA  
 <213> Mouse Intracisternal A-particle

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 accaactgca agcagtggtta ccagaggaag atctgcggca agtcgacagt catcagttat 180  
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 ctctcaaadc tgtatgagac catgggagtt gtgggatcga ccaccacaca gctgtataca 300  
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 gtcaacatcg aactgctcaa tgctctccgc taccacatgg tggacaggcg ggtcctgacc 480



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<210> 5  
<211> 609

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<212>    PRT
<213>    Mouse Intracisternal A-particle

<220>
<221>    PEPTIDE
<222>    (1)..(609)
<223>    23 to 641 amino acid sequence of mouse

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  1              5              10              15

Leu Arg Gly Arg Gln His Gly Pro Asn Val Cys Ala Val Gln Lys Val
      20              25              30

Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn Cys Lys Gln Trp Tyr Gln
      35              40              45

Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys Cys Pro
      50              55              60

Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala Leu Pro
      65              70              75              80

Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr Thr Thr
      85              90              95

Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met Glu Gly
      100              105              110

Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp Ala Ser
      115              120              125

Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn Ile Glu
      130              135              140

Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val Leu Thr
      145              150              155              160

Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln Asn Ser
      165              170              175

Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val Asn Cys
      180              185              190

Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val Val His
      195              200              205

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Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln Gln Ile  
 210 215 220

Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val Ala Ala  
 225 230 235 240

Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr Leu Leu  
 245 250 255

Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr Leu Asn  
 260 265 270

Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn Asn His  
 275 280 285

Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly Leu Ser  
 290 295 300

Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser Gly Asp  
 305 310 315 320

Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp Ile Leu  
 325 330 335

Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile Pro Asp  
 340 345 350

Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val Ser Thr  
 355 360 365

Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu Ser Gly  
 370 375 380

Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe Lys Asp  
 385 390 395 400

Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg Asn His  
 405 410 415

Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly Gln Thr  
 420 425 430

Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr Arg Asn  
 435 440 445

Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys Arg Gly  
 450 455 460

Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro Pro Met  
465 470 475 480

Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu  
485 490 495

Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu  
500 505 510

Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu  
515 520 525

Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala  
530 535 540

Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly  
545 550 555 560

Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu  
565 570 575

Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala  
580 585 590

Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn  
595 600 605

Val

<210> 6  
<211> 391  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Betaig-h3 D-IV

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catggagatc ctcaaccggg aaggggtcta cactgttttt gctcccacca atgaagcggt 180  
ccaagccatg cctccagaag aactgaacaa actcttggca aatgccaagg aacttaccaa 240

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catcctgaag taccacattg gtgatgaaat cctgggttagc ggaggcatcg gggccctggg      300
gcggctgaag tctctccaag gggacaaact ggaagtcagc tcgaaaaaca atgtagtgag      360
tgtcaataag gagcctgttg ccgaaaccga c                                     391

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<210>      7
<211>     140
<212>      PRT
<213>      Artificial Sequence

<220>
<223>      Betaig-h3 D-IV(1X) amino acid sequence

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Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
          20              25              30

Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
          35              40              45

Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
          50              55              60

Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
          65              70              75              80

Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
          85              90              95

Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
          100              105              110

Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
          115              120              125

His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn
          130              135              140

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<210>      8
<211>     280
<212>      PRT
<213>      Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Betaig-h3 D-IV(2X) amino acid sequence

&lt;400&gt; 8

Leu	Thr	Pro	Pro	Met	Gly	Thr	Val	Met	Asp	Val	Leu	Lys	Gly	Asp	Asn
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Arg	Phe	Ser	Met	Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu
			20					25					30		

Thr	Leu	Asn	Arg	Glu	Gly	Val	Tyr	Thr	Val	Phe	Ala	Pro	Thr	Asn	Glu
		35					40					45			

Ala	Phe	Arg	Ala	Leu	Pro	Pro	Arg	Glu	Arg	Ser	Arg	Leu	Leu	Gly	Asp
	50						55				60				

Ala	Lys	Glu	Leu	Ala	Asn	Ile	Leu	Lys	Tyr	His	Ile	Gly	Asp	Glu	Ile
65					70					75				80	

Leu	Val	Ser	Gly	Gly	Ile	Gly	Ala	Leu	Val	Arg	Leu	Lys	Ser	Leu	Gln
				85					90					95	

Gly	Asp	Lys	Leu	Glu	Val	Ser	Leu	Lys	Asn	Asn	Val	Val	Ser	Val	Asn
			100					105					110		

Lys	Glu	Pro	Val	Ala	Glu	Pro	Asp	Ile	Met	Ala	Thr	Asn	Gly	Val	Val
		115					120					125			

His	Val	Ile	Thr	Asn	Val	Leu	Gln	Pro	Pro	Ala	Asn	Leu	Thr	Pro	Pro
	130					135					140				

Met	Gly	Thr	Val	Met	Asp	Val	Leu	Lys	Gly	Asp	Asn	Arg	Phe	Ser	Met
145					150					155					160

Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu	Thr	Leu	Asn	Arg
				165					170					175	

Glu	Gly	Val	Tyr	Thr	Val	Phe	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Arg	Ala
			180					185					190		

Leu	Pro	Pro	Arg	Glu	Arg	Ser	Arg	Leu	Leu	Gly	Asp	Ala	Lys	Glu	Leu
		195					200					205			

Ala	Asn	Ile	Leu	Lys	Tyr	His	Ile	Gly	Asp	Glu	Ile	Leu	Val	Ser	Gly
	210					215				220					

Gly	Ile	Gly	Ala	Leu	Val	Arg	Leu	Lys	Ser	Leu	Gln	Gly	Asp	Lys	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

225                      230                      235                      240  
 Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val  
                                  245                      250                      255  
 Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr  
                                  260                      265                      270  
 Asn Val Leu Gln Pro Pro Ala Asn  
                                  275                      280

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 <211>    420  
 <212>    PRT  
 <213>    Artificial Sequence

<220>  
 <223>    Betaig-h3 D-IV(3X) amino acid sequence

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 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu  
                                  20                      25                      30  
 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu  
                                  35                      40                      45  
 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp  
   50                      55                      60  
 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile  
   65                      70                      75                      80  
 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln  
                                  85                      90                      95  
 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn  
                                  100                      105                      110  
 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val  
                                  115                      120                      125  
 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro  
   130                      135                      140

Met Gly Thr Val	Met Asp Val	Leu Lys Gly	Asp Asn Arg	Phe Ser Met
145	150	155		160
Leu Val Ala Ala	Ile Gln Ser	Ala Gly Leu	Thr Glu Thr	Leu Asn Arg
	165	170		175
Glu Gly Val Tyr	Thr Val Phe	Ala Pro Thr	Asn Glu Ala	Phe Arg Ala
	180	185		190
Leu Pro Pro Arg	Glu Arg Ser	Arg Leu Leu	Gly Asp Ala	Lys Glu Leu
	195	200		205
Ala Asn Ile Leu	Lys Tyr His	Ile Gly Asp	Glu Ile Leu	Val Ser Gly
	210	215		220
Gly Ile Gly Ala	Leu Val Arg	Leu Lys Ser	Leu Gln Gly	Asp Lys Leu
225	230		235	240
Glu Val Ser Leu	Lys Asn Asn	Val Val Ser	Val Asn Lys	Glu Pro Val
	245		250	255
Ala Glu Pro Asp	Ile Met Ala	Thr Asn Gly	Val Val His	Val Ile Thr
	260		265	270
Asn Val Leu Gln	Pro Pro Ala	Asn Leu Thr	Pro Pro Met	Gly Thr Val
	275	280		285
Met Asp Val Leu	Lys Gly Asp	Asn Arg Phe	Ser Met Leu	Val Ala Ala
	290	295		300
Ile Gln Ser Ala	Gly Leu Thr	Glu Thr Leu	Asn Arg Glu	Gly Val Tyr
305		310		320
Thr Val Phe Ala	Pro Thr Asn	Glu Ala Phe	Arg Ala Leu	Pro Pro Arg
	325		330	335
Glu Arg Ser Arg	Leu Leu Gly	Asp Ala Lys	Glu Leu Ala	Asn Ile Leu
	340		345	350
Lys Tyr His Ile	Gly Asp Glu	Ile Leu Val	Ser Gly Gly	Ile Gly Ala
	355		360	365
Leu Val Arg Leu	Lys Ser Leu	Gln Gly Asp	Lys Leu Glu	Val Ser Leu
	370	375		380
Lys Asn Asn Val	Val Ser Val	Asn Lys Glu	Pro Val Ala	Glu Pro Asp
385		390		400
Ile Met Ala Thr	Asn Gly Val	Val His Val	Ile Thr Asn	Val Leu Gln





Glu	Gly	Val	Tyr	Thr	Val	Phe	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Arg	Ala
180						185						190			
Leu	Pro	Pro	Arg	Glu	Arg	Ser	Arg	Leu	Leu	Gly	Asp	Ala	Lys	Glu	Leu
195						200						205			
Ala	Asn	Ile	Leu	Lys	Tyr	His	Ile	Gly	Asp	Glu	Ile	Leu	Val	Ser	Gly
210						215						220			
Gly	Ile	Gly	Ala	Leu	Val	Arg	Leu	Lys	Ser	Leu	Gln	Gly	Asp	Lys	Leu
225			230						235			240			
Glu	Val	Ser	Leu	Lys	Asn	Asn	Val	Val	Ser	Val	Asn	Lys	Glu	Pro	Val
			245						250			255			
Ala	Glu	Pro	Asp	Ile	Met	Ala	Thr	Asn	Gly	Val	Val	His	Val	Ile	Thr
			260						265			270			
Asn	Val	Leu	Gln	Pro	Pro	Ala	Asn	Leu	Thr	Pro	Pro	Met	Gly	Thr	Val
275						280						285			
Met	Asp	Val	Leu	Lys	Gly	Asp	Asn	Arg	Phe	Ser	Met	Leu	Val	Ala	Ala
290						295						300			
Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu	Thr	Leu	Asn	Arg	Glu	Gly	Val	Tyr
305			310						315			320			
Thr	Val	Phe	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Arg	Ala	Leu	Pro	Pro	Arg
			325						330			335			
Glu	Arg	Ser	Arg	Leu	Leu	Gly	Asp	Ala	Lys	Glu	Leu	Ala	Asn	Ile	Leu
			340			345						350			
Lys	Tyr	His	Ile	Gly	Asp	Glu	Ile	Leu	Val	Ser	Gly	Gly	Ile	Gly	Ala
355						360						365			
Leu	Val	Arg	Leu	Lys	Ser	Leu	Gln	Gly	Asp	Lys	Leu	Glu	Val	Ser	Leu
370						375						380			
Lys	Asn	Asn	Val	Val	Ser	Val	Asn	Lys	Glu	Pro	Val	Ala	Glu	Pro	Asp
385			390						395			400			
Ile	Met	Ala	Thr	Asn	Gly	Val	Val	His	Val	Ile	Thr	Asn	Val	Leu	Gln
			405						410			415			
Pro	Pro	Ala	Asn	Leu	Thr	Pro	Pro	Met	Gly	Thr	Val	Met	Asp	Val	Leu
			420			425						430			
Lys	Gly	Asp	Asn	Arg	Phe	Ser	Met	Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala

435		440		445
Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala				
450		455		460
Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg				
465		470		475 480
Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile				
	485		490	495
Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu				
	500		505	510
Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val				
	515		520	525
Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr				
	530		535	540
Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn				
545		550		555 560

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 Asn Lys Asp Ile Leu  
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 Glu Pro Asp Ile  
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